

**AMENDMENTS TO THE SPECIFICATION**

In the specification:

Please replace the paragraph beginning at page 1, line 5 with the following paragraph:

Related Patent Applications

This application is a continuation application of serial no 08/573, filed on December 18, 1995, abandoned pending. The contents of the aforementioned application are hereby incorporated by reference.

Please replace the paragraph at page 6, line 36 through page 7, line 10 with the following paragraph:

A particularly preferred peptide library for use in the methods of the invention is an anchor library as described in U.S. Patent Application Serial No. 6,475,806 [[ ]]entitled *Anchor Libraries and Identification of Peptide Binding Sequences*, filed on June 5, 1995 (attorney docket number: P0567/7000), the entire contents of which are expressly incorporated herein by reference. As used herein, the term "anchor library" refers to a peptide library in which the peptides have non-continuous regions of random amino acids separated by specifically designated amino acid residues. Anchor libraries are therefore subsets of a complete library of a specified length. Anchor libraries can be used to identify essential contacts between a ligand and a target, and have the advantage that only a subset of all possible peptides need be synthesized and screened. In a preferred embodiment, an anchor library is made up of peptides about 16 amino acids long. An anchor library can be prepared by genetic means (e.g., by synthesizing a multiplicity of nucleic acid molecules encoding a multiplicity of anchor peptides)

a2  
or by chemical means (e.g., by directly synthesizing a multiplicity of anchor peptides).

L Please replace the paragraph appearing at page 12, line 29 through line 36 with the following paragraph:

a3  
A phage anchor library comprising a multiplicity of peptides is used as the first library in the method. The anchor library is comprised of peptides having random amino acid residues distributed throughout domains of alanine (Ala) and/or glycine (Gly) residues. For example, the anchor library can be composed of peptides that are sixteen amino acid residues in length and have the amino acid sequence:

$X^1(\text{Ala/Gly})_4X^2(\text{Ala/Gly})_4X^3(\text{Ala/Gly})_4X^4$  (SEQ ID NO: 1)

wherein  $X^1$ ,  $X^2$ ,  $X^3$  and  $X^4$  can be any amino acid residue and each can be the same or different from the others.

L Please replace the paragraph appearing at page 14, line 27 through page 15, line 4 with the following paragraph:

a4  
After obtaining the DNA sequences encoding the selected peptides, the DNA sequences are optimally aligned to generate a peptide motif. The peptide motif is determined from the amino acid residues that are conserved in at least two of the selected peptides. For example, if biopanning of the anchor library leads to selection of four peptides having the following amino acid sequences (standard three-letter abbreviations are used for amino acids):

Ser-(Ala/Gly)<sub>4</sub>-Arg-(Ala/Gly)<sub>4</sub>-Leu-(Ala/Gly)<sub>4</sub>-Met (SEQ ID NO: 2)

Ser-(Ala/Gly)<sub>4</sub>-Lys-(Ala/Gly)<sub>4</sub>-Leu-(Ala/Gly)<sub>4</sub>-Gln (SEQ ID NO: 3)

Phe-(Ala/Gly)<sub>4</sub>-Arg-(Ala/Gly)<sub>4</sub>-Leu-(Ala/Gly)<sub>4</sub>-Thr (SEQ ID NO: 4)

Ser-(Ala/Gly)<sub>4</sub>-Asn-(Ala/Gly)<sub>4</sub>-Leu-(Ala/Gly)<sub>4</sub>-Ile (SEQ ID NO: 5)

a peptide motif can be generated having the amino acid sequence:

Ser-(Ala/Gly)<sub>4</sub>-Arg-(Ala/Gly)<sub>4</sub>-Leu-(Ala/Gly)<sub>4</sub>-Xaa (SEQ ID NO: 6)

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cont

(wherein Xaa can be any amino acid residue).

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